

Sequence Listing

<110> Baker, Kevin
 Botstein, David
 Eaton, Dan
 Ferrara, Napoleone
 Filvaroff, Ellen
 Gerritsen, Mary
 Goddard, Audrey
 Godowski, Paul
 Grimaldi, Christopher
 Gurney, Austin
 Hillan, Kenneth
 Kljavin, Ivar
 Napier, Mary
 Roy, Margaret
 Tumas, Daniel
 Wood, William

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME

<130> P2548P1C1

<150> 60/067,411

<151> December 3, 1997

<150> 60/069,334

<151> December 11, 1997

<150> 60/069335

<151> December 11, 1997

<150> 60/069,278

<151> December 11, 1997

<150> 60/069,425

<151> December 12, 1997

<150> 60/069,696

<151> December 16, 1997

<150> 60/069,694

<151> December 16, 1997

<150> 60/069,702

<151> December 16, 1997

<150> 60/069,870

<151> December 17, 1997

<150> 60/069,873

<151> December 17, 1997

<150> 60/068,017

<151> December 18, 1997

<150> 60/070,440

100E90" 2E44660

FOUOESD" ZC444660

<151> January 5, 1998
<150> 60/074,086
<151> February 9, 1998
<150> 60/074,092
<151> February 9, 1998
<150> 60/075,945
<151> February 25, 1998
<150> 60/112,850
<151> December 16, 1998
<150> 60/113,296
<151> December 22, 1998
<150> 60/146,222
<151> July 28, 1999
<150> PCT/US98/19330
<151> September 16, 1998
<150> PCT/US98/25108
<151> December 1, 1998
<150> 09/216,021
<151> December 16, 1998
<150> 09/218,517
<151> December 22, 1998
<150> 09/254,311
<151> March 3, 1999
<150> PCT/US99/12252
<151> June 22, 1999
<150> PCT/US99/21090
<151> September 15, 1999
<150> PCT/US99/28409
<151> November 30, 1999
<150> PCT/US99/28313
<151> November 30, 1999
<150> PCT/US99/28301
<151> December1, 1999
<150> PCT/US99/30095
<151> December 16, 1999
<150> PCT/US00/03565
<151> February 11, 2000
<150> PCT/US00/04414
<151> February 22, 2000

<150> PCT/US00/05841
 <151> March 2, 2000

<150> PCT/US00/08439
 <151> March 30, 2000

<150> PCT/US00/14042
 <151> May 22, 2000

<150> PCT/US00/20710
 <151> July 28, 2000

<150> PCT/US00/32678
 <151> December 1, 2000

<150> PCT/US01/06520
 <151> February 28, 2001

<160> 120

<210> 1
 <211> 2454
 <212> DNA
 <213> Homo Sapien

<400> 1
 ggactaatct gtgggagcag tttattccag tatcaccag ggtgcagcca 50
 caccaggact gtgttgaagg gtgttttttt ttttttaaata gtaatacctc 100
 ctcacttttt cttcttacac agtgtctgag aacattttaca ttatagataa 150
 gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
 cagtcctaga ctggtcttct acactaagac accatgaagg agtatgtgct 250
 cctattattc ctggctttgt gctctgccaa acccttcttt agcccttcac 300
 acatcgact gaagaatatg atgctgaagg atatggaaga cacagatgat 350
 gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
 tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
 tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
 ttaggtttga cctcagtcac aaccaacatt ccatttgata ctgaatgct 550
 tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600
 gactcacttc actttatggt ctgacctga acaacaacaa gctaacgaag 650
 attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
 gtcccacaat caactaagt aaataccact taatcttccc aaatcattag 750
 cagaactcag aattcatgaa aataaagtta agaaaatata aaaggacaca 800

aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
tagtataact gaataagcag agcatcaaat taaacagaca gaaaccgaaa 2350
gctctatata aatgctcaga gttctttatg tatttcttat tggcattcaa 2400
catatgtaaa atcagaaaac agggaaattt tcattaaaaa tattggtttg 2450
aaat 2454

```
<210> 2
<211> 379
<212> PRT
<213> Homo Sapien
```

Ile	Glu	Pro	Gly	Ala	Phe	Glu	Gly	Val	Thr	Val	Phe	His	Ile	Arg
				215					220					225
Ile	Ala	Glu	Ala	Lys	Leu	Thr	Ser	Val	Pro	Lys	Gly	Leu	Pro	Pro
				230					235					240
Thr	Leu	Leu	Glu	Leu	His	Leu	Asp	Tyr	Asn	Lys	Ile	Ser	Thr	Val
				245					250					255
Glu	Leu	Glu	Asp	Phe	Lys	Arg	Tyr	Lys	Glu	Leu	Gln	Arg	Leu	Gly
				260					265					270
Leu	Gly	Asn	Asn	Lys	Ile	Thr	Asp	Ile	Glu	Asn	Gly	Ser	Leu	Ala
				275					280					285
Asn	Ile	Pro	Arg	Val	Arg	Glu	Ile	His	Leu	Glu	Asn	Asn	Lys	Leu
				290					295					300
Lys	Lys	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Leu	Lys	Tyr	Leu	Gln	Ile
				305					310					315
Ile	Phe	Leu	His	Ser	Asn	Ser	Ile	Ala	Arg	Val	Gly	Val	Asn	Asp
				320					325					330
Phe	Cys	Pro	Thr	Val	Pro	Lys	Met	Lys	Lys	Ser	Leu	Tyr	Ser	Ala
				335					340					345
Ile	Ser	Leu	Phe	Asn	Asn	Pro	Val	Lys	Tyr	Trp	Glu	Met	Gln	Pro
				350					355					360
Ala	Thr	Phe	Arg	Cys	Val	Leu	Ser	Arg	Met	Ser	Val	Gln	Leu	Gly
				365					370					375
Asn	Phe	Gly	Met											

<210> 3
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 3
 ggaaatgagt gcaaaccctc 20

<210> 4
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 4
 tccaagctg aacactcatt ctgc 24

<210> 5
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 5
gggtgacggt gttccatata agaattgcag aagcaaaact gacctcagtt 50

<210> 6
<211> 3441
<212> DNA
<213> Homo Sapien

<400> 6
cggacgcgtg ggcggaacgc tgggcccgcg gcaccgcccc cggcccggcc 50
ctccgccctc cgcaactcgc cctccctccc tccgcccgtt cccgcgccct 100
cctccctccc tctcccccag ctgtcccgtt cgcgtcatgc cgagcctccc 150
ggccccgcgc gcccgcgtgc tgetectcgg gctgctgctg ctcggtccc 200
ggcgggcccc cggcgccggc ccagagcccc ccgtgctgcc catccgttct 250
gagaaggagc cgctgcccgt tcggggagcg gcaggtgca ccttcggcgg 300
gaaggcttat gccttggacg agacgtggca cccggacctt gggcagccat 350
tcgggggtgat gcgtgcgtg ctgtgcgcct gcgaggcgcc tcagtggggt 400
cgccgtacca ggggccctgg cagggtcagc tgcaagaaca tcaaaccaga 450
gtgcccaacc ccggcctgtg ggcagccgcg ccagctgccg ggacactgct 500
gccagacctg cccccaggag cgcagcagtt cggagcggca gccgagcggc 550
ctgtccttcg agtatccgcg ggaccgcggag catcgcagtt atagcgaccg 600
cggggagcca ggcgctgagg agcgggcccc tgggtgacggc cacacggact 650
tcgtggcgct gctgacaggg ccgaggtcgc aggcggtggc acgagcccga 700
gtctcgtgc tgcgctctag cctccgcttc tctatctcct acaggcggct 750
ggaccgcctt accaggatcc gcttctcaga ctccaatggc agtgctctgt 800
ttgagcacc cgcagcccc acccaagatg gcctggtctg tggggtgtgg 850
cgggcagtgc ctcggttgct tctgcccgtc cttagggcag aacagctgca 900
tgtggcactt gtgacctca ctcacccttc aggggaggtc tgggggcctc 950
tcatccggca ccgggccctg gctgcagaga ccttcagtgc catcctgact 1000
ctagaaggcc cccacagca gggcgtaggg ggcatcacc tgctcactct 1050

FOOEBD"2E444660

cagtgcacaca gaggactcct tgcatttttt gctgctcttc cgagggtgc 1100
 tggaaccag gagtggggga ctaaccaggt ttcccttgag gctccagatt 1150
 ctacaccaggg ggcagctact gcgagaactt caggccaatg tctcagccca 1200
 ggaaccagggc tttgctgagg tgctgcccga cctgacagtc caggagatgg 1250
 actggctggg gctgggggag ctgcagatgg ccctggagtg ggcaggcagg 1300
 ccagggtgc gcatcagtg acacattgct gccaggaaga gctgcgacgt 1350
 cctgcaaagt gtcccttggt gggctgatgc cctgatccca gtccagacgg 1400
 gtgctgccgg ctcagccagc ctcacgtgc taggaaatgg ctccctgatc 1450
 tatcaggtgc aagtggtagg gacaagcagt gaggtggtag ccatgacact 1500
 ggagaccaag cctcagcggg gggatcagcg cactgtcctg tgccacatgg 1550
 ctggactcca gccaggagga cacacggcgg tgggtatctg ccctgggctg 1600
 ggtgcccag gggctcatat gctgctgcag aatgagctct tccctgaacgt 1650
 gggcaccaag gacttcccag acggagagct tcgggggcac gtggctgccc 1700
 tgccctactg tgggcatagc gcccgccatg acacgctgcc cgtgccccta 1750
 gcaggagccc tgggtgctacc ccctgtgaag agccaagcag cagggcacgc 1800
 ctggctttcc ttggataccc actgtcacct gcactatgaa gtgctgctgg 1850
 ctgggcttgg tggtcagaa caaggcactg tccctgccc cctccttggg 1900
 cctcctggaa cgcaggggc tcggcggctg ctgaagggat tctatggctc 1950
 agaggcccag ggtgtggtga aggacctgga gccggaactg ctgcggcacc 2000
 tggcaaaagg catggcctcc ctgatgatca ccaccaaggg tagccccaga 2050
 ggggagctcc gagggcaggt gcacatagcc aaccaatgtg aggttggcgg 2100
 actgcgctg gaggcggccg gggccgaggg ggtgcgggctg ctgggggctc 2150
 cggatacagc ctctgctgcg ccgcctgtgg tgctggtct cccggcccta 2200
 gcgcccgcga aacctgggtg tccctgggcg ccccgagacc ccaacacatg 2250
 cttcttcgag gggcagcagc gccccacgg ggctcgctgg gcgcccact 2300
 acgacctgct ctgctcactc tgcacctgcc agagacgaac ggtgatctgt 2350
 gacctgggtg tgtgcccacc gccagctgc ccacaccggg tgcaggctcc 2400
 cgaccagtgc tgccctgttt gccctgagaa acaagatgtc agagacttgc 2450
 cagggtgcc aaggagccgg gaccagggg agggctgcta ttttgatgg 2500

gaccggagct	ggcgggcagc	gggtacgcgg	tggcaccccg	ttgtgcccc	2550
ctttggctta	attaagtgtg	ctgtctgcac	ctgcaagggg	ggcactggag	2600
aggtgcactg	tgagaagggtg	cagtgtcccc	ggctggcctg	tgcccagcct	2650
gtgctgttca	accccaccga	ctgctgcaaa	cagtgtccag	tggggtcggg	2700
ggcccccccc	cagctggggg	accccatgca	ggctgatggg	ccccggggct	2750
gccgttttgc	tgggcagtgg	ttcccagaga	gtcagagctg	gcacccctca	2800
gtgccccctt	ttggagagat	gagctgtatc	acctgcagat	gtggggcagg	2850
ggtgcctcac	tgtgagcggg	atgactgttc	actgccactg	tcctgtggct	2900
cggggaagga	gagtcgatgc	tgttcccgct	gcacggccca	ccggcggccc	2950
ccagagacca	gaactgatcc	agagctggag	aaagaagccg	aaggctctta	3000
gggagcagcc	agagggccaa	gtgaccaaga	ggatggggcc	tgagctgggg	3050
aaggggtggc	atcgaggacc	ttcttgcatt	ctcctgtggg	aagcccagtg	3100
cctttgctcc	tctgtcctgc	ctctactccc	acccccacta	cctctgggaa	3150
ccacagctcc	acaaggggga	gaggcagctg	ggccagaccg	aggtcacagc	3200
cactccaagt	cctgccttgc	caccctcggc	ctctgtcctg	gaagccccac	3250
ccctttcttc	ctgtacataa	tgtcactggc	ttgttgggat	ttttaattta	3300
tcttactca	gcaccaaggg	cccccgacac	tccactcctg	ctgcccctga	3350
gctgagcaga	gtcattattg	gagagttttg	tatttattaa	aacatttctt	3400
tttcagtcaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	a	3441

<210> 7

<400> 7

FOUO "2E44660"

Arg	Cys	Val	Leu	Cys	Ala	Cys	Glu	Ala	Pro	Gln	Trp	Gly	Arg	Arg	
				80					85					90	
Thr	Arg	Gly	Pro	Gly	Arg	Val	Ser	Cys	Lys	Asn	Ile	Lys	Pro	Glu	
				95					100					105	
Cys	Pro	Thr	Pro	Ala	Cys	Gly	Gln	Pro	Arg	Gln	Leu	Pro	Gly	His	
				110					115					120	
Cys	Cys	Gln	Thr	Cys	Pro	Gln	Glu	Arg	Ser	Ser	Ser	Glu	Arg	Gln	
				125					130					135	
Pro	Ser	Gly	Leu	Ser	Phe	Glu	Tyr	Pro	Arg	Asp	Pro	Glu	His	Arg	
				140					145					150	
Ser	Tyr	Ser	Asp	Arg	Gly	Glu	Pro	Gly	Ala	Glu	Glu	Arg	Ala	Arg	
				155					160					165	
Gly	Asp	Gly	His	Thr	Asp	Phe	Val	Ala	Leu	Leu	Thr	Gly	Pro	Arg	
				170					175					180	
Ser	Gln	Ala	Val	Ala	Arg	Ala	Arg	Val	Ser	Leu	Leu	Arg	Ser	Ser	
				185					190					195	
Leu	Arg	Phe	Ser	Ile	Ser	Tyr	Arg	Arg	Leu	Asp	Arg	Pro	Thr	Arg	
				200					205					210	
Ile	Arg	Phe	Ser	Asp	Ser	Asn	Gly	Ser	Val	Leu	Phe	Glu	His	Pro	
				215					220					225	
Ala	Ala	Pro	Thr	Gln	Asp	Gly	Leu	Val	Cys	Gly	Val	Trp	Arg	Ala	
				230					235					240	
Val	Pro	Arg	Leu	Ser	Leu	Arg	Leu	Leu	Arg	Ala	Glu	Gln	Leu	His	
				245					250					255	
Val	Ala	Leu	Val	Thr	Leu	Thr	His	Pro	Ser	Gly	Glu	Val	Trp	Gly	
				260					265					270	
Pro	Leu	Ile	Arg	His	Arg	Ala	Leu	Ala	Ala	Glu	Thr	Phe	Ser	Ala	
				275					280					285	
Ile	Leu	Thr	Leu	Glu	Gly	Pro	Pro	Gln	Gln	Gly	Val	Gly	Gly	Ile	
				290					295					300	
Thr	Leu	Leu	Thr	Leu	Ser	Asp	Thr	Glu	Asp	Ser	Leu	His	Phe	Leu	
				305					310					315	
Leu	Leu	Phe	Arg	Gly	Leu	Leu	Glu	Pro	Arg	Ser	Gly	Gly	Leu	Thr	
				320					325					330	
Gln	Val	Pro	Leu	Arg	Leu	Gln	Ile	Leu	His	Gln	Gly	Gln	Leu	Leu	
				335					340					345	
Arg	Glu	Leu	Gln	Ala	Asn	Val	Ser	Ala	Gln	Glu	Pro	Gly	Phe	Ala	
				350					355					360	
Glu	Val	Leu	Pro	Asn	Leu	Thr	Val	Gln	Glu	Met	Asp	Trp	Leu	Val	

365										370					375				
Leu	Gly	Glu	Leu	Gln	Met	Ala	Leu	Glu	Trp	Ala	Gly	Arg	Pro	Gly					
				380					385					390					
Leu	Arg	Ile	Ser	Gly	His	Ile	Ala	Ala	Arg	Lys	Ser	Cys	Asp	Val					
				395					400					405					
Leu	Gln	Ser	Val	Leu	Cys	Gly	Ala	Asp	Ala	Leu	Ile	Pro	Val	Gln					
				410					415					420					
Thr	Gly	Ala	Ala	Gly	Ser	Ala	Ser	Leu	Thr	Leu	Leu	Gly	Asn	Gly					
				425					430					435					
Ser	Leu	Ile	Tyr	Gln	Val	Gln	Val	Val	Gly	Thr	Ser	Ser	Glu	Val					
				440					445					450					
Val	Ala	Met	Thr	Leu	Glu	Thr	Lys	Pro	Gln	Arg	Arg	Asp	Gln	Arg					
				455					460					465					
Thr	Val	Leu	Cys	His	Met	Ala	Gly	Leu	Gln	Pro	Gly	Gly	His	Thr					
				470					475					480					
Ala	Val	Gly	Ile	Cys	Pro	Gly	Leu	Gly	Ala	Arg	Gly	Ala	His	Met					
				485					490					495					
Leu	Leu	Gln	Asn	Glu	Leu	Phe	Leu	Asn	Val	Gly	Thr	Lys	Asp	Phe					
				500					505					510					
Pro	Asp	Gly	Glu	Leu	Arg	Gly	His	Val	Ala	Ala	Leu	Pro	Tyr	Cys					
				515					520					525					
Gly	His	Ser	Ala	Arg	His	Asp	Thr	Leu	Pro	Val	Pro	Leu	Ala	Gly					
				530					535					540					
Ala	Leu	Val	Leu	Pro	Pro	Val	Lys	Ser	Gln	Ala	Ala	Gly	His	Ala					
				545					550					555					
Trp	Leu	Ser	Leu	Asp	Thr	His	Cys	His	Leu	His	Tyr	Glu	Val	Leu					
				560					565					570					
Leu	Ala	Gly	Leu	Gly	Gly	Ser	Glu	Gln	Gly	Thr	Val	Thr	Ala	His					
				575					580					585					
Leu	Leu	Gly	Pro	Pro	Gly	Thr	Pro	Gly	Pro	Arg	Arg	Leu	Leu	Lys					
				590					595					600					
Gly	Phe	Tyr	Gly	Ser	Glu	Ala	Gln	Gly	Val	Val	Lys	Asp	Leu	Glu					
				605					610					615					
Pro	Glu	Leu	Leu	Arg	His	Leu	Ala	Lys	Gly	Met	Ala	Ser	Leu	Met					
				620					625					630					
Ile	Thr	Thr	Lys	Gly	Ser	Pro	Arg	Gly	Glu	Leu	Arg	Gly	Gln	Val					
				635					640					645					
His	Ile	Ala	Asn	Gln	Cys	Glu	Val	Gly	Gly	Leu	Arg	Leu	Glu	Ala					
				650					655					660					

Ala Gly Ala Glu Gly Val Arg Ala Leu Gly Ala Pro Asp Thr Ala	665	670	675
Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu Ala Pro	680	685	690
Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys	695	700	705
Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro	710	715	720
Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr	725	730	735
Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His	740	745	750
Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys	755	760	765
Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro	770	775	780
Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala	785	790	795
Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys	800	805	810
Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys	815	820	825
Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg	830	835	840
Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly	845	850	855
Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg	860	865	870
Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp	875	880	885
His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys	890	895	900
Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser	905	910	915
Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser	920	925	930
Arg Cys Thr Ala His Arg Arg Pro Pro Glu Thr Arg Thr Asp Pro	935	940	945
Glu Leu Glu Lys Glu Ala Glu Gly Ser			

<210> 13

[illegible]

```
<400> 13
gcaggggtgct caaacaggac ac 22
```

```
<210> 14
<211> 3231
<212> DNA
<213> Homo Sapien
```

```
<400> 14
ggcggagcag ccctagccgc caccgtcgct ctgcagctc tcgtcgccac 50
tgccaccgcc gccgccgtca ctgcgtcctg gtcccggctc ccgcgccctc 100
ccggccggcc atgcagcccc gccgcgccca ggcgcccggt gcgcagctgc 150
tgcccgcgct ggccctgctg ctgctgctgc tcggagcggg gccccgaggg 200
agctccctgg ccaacccggt gccgcgcgcg cccttgtctg cgcccgggcc 250
gtgcgcgcgc cagccctgcc ggaatggggg tgtgtgcacc tcgcgccttg 300
agccggaccc gcagcacccg gccccgcgcg gcgagcctgg ctacagctgc 350
acctgccccg ccgggatctc cggcgccaac tgccagcttg ttgcagatcc 400
ttgtgccagc aacccttgtc accatggcaa ctgcagcagc agcagcagca 450
gcagcagcga tggctacctc tgcatttgca atgaaggcta tgaaggctcc 500
aactgtgaac aggcacttcc cagtctccca gccactggct ggaccgaatc 550
catggcacc cagacagcttc agcctgttcc tgctactcag gagcctgaca 600
aaatcctgcc tcgctctcag gcaacggtga cactgcctac ctggcagccg 650
aaaacagggc agaaagtgtg agaaatgaaa tgggatcaag tggaggtgat 700
cccagatatt gcctgtggga atgccagttc taacagctct gcgggtggcc 750
gcctgggtatc ctttgaagtg ccacagaaca cctcagtcaa gattcggcaa 800
gatgccactg cctcactgat tttgctctgg aaggtcacgg ccacaggatt 850
ccaacagtgc tcctcatag atggacgaag tgtgaccccc cttcaggctt 900
caggggggact ggtcctcctg gaggagatgc tcgccttggg gaataatcac 950
tttattgggt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000
cttaactctg qtqgtgaagg tcaqcacctg tqtgccgggg gagaqtcacg 1050
```

caaatgactt ggagtgttca ggaaaaggaa aatgcaccac gaagccgtca 1100
 gaggcaactt tttcctgtac ctgtgaggag cagtacgtgg gtactttctg 1150
 tgaagaatac gatgcttgcc agaggaaacc ttgccaaaac aacgcgagct 1200
 gtattgatgc aaatgaaaag caagatggga gcaatttcac ctgtgtttgc 1250
 cttcctgggt atactggaga gctttgccag tccaagattg attactgcat 1300
 cctagacca tgcagaaatg gagcaacatg catttccagt ctcagtggat 1350
 tcacctgcca gtgtccagaa ggatacttcg gatctgcttg tgaagaaaag 1400
 gtggaccctt gcgcctcgtc tccgtgccag aacaacggca cctgctatgt 1450
 ggacggggta cactttacct gcaactgcag cccgggcttc acagggccga 1500
 cctgtgcca gcttattgac ttctgtgccc tcagcccctg tgctcatggc 1550
 acgtgccgca gcgtgggcac cagctacaaa tgctctgtg atccagggtta 1600
 ccatggcctc tactgtgagg aggaatataa tgagtgcctc tccgtccat 1650
 gcctgaatgc agccacctgc agggacctcg ttaatggcta tgagtgtgtg 1700
 tgctggcag aatacaaagg aacacactgt gaattgtaca aggatccctg 1750
 cgtaacgtc agctgtctga acggagccac ctgtgacagc gacggcctga 1800
 atggcacgtg catctgtgca cccgggttta cagggaaga gtgcgacatt 1850
 gacataaatg aatgtgacag taaccctgc caccatggtg ggagctgcct 1900
 ggaccagccc aatggttata actgccactg cccgcatggt tgggtgggag 1950
 caaactgtga gatccacctc caatggaagt ccgggcacat ggcgagagc 2000
 ctcaccaaca tgccacggca ctccctctac atcatcattg gagccctctg 2050
 cgtggccttc atccttatgc tgatcatcct gatcgtggg atttgccgca 2100
 tcagccgcat tgaataccag ggttcttcca ggccagccta tgaggagtgc 2150
 tacaactgcc gcagcatcga cagcgagtgc agcaatgcc ttgcatccat 2200
 ccggcatgcc aggtttggaa agaaatcccg gcctgcaatg tatgatgtga 2250
 gccccatgc ctatgaagat tacagtctg atgacaaacc cttggtcaca 2300
 ctgattaaaa ctaaagattt gtaatctttt tttggattat ttttcaaaa 2350
 gatgagatac tacactcatt taaatatttt taagaaaata aaaagcttaa 2400
 gaaattttaa atgctagctg ctcaagagtt ttcagtagaa tatttaagaa 2450
 ctaattttct gcagctttta gtttggaata aatattttta aaacaaaatt 2500

tgtgaaacct	atagacgatg	ttttaatgta	ccttcagctc	tctaaactgt	2550
gtgcttctac	tagtgtgtgc	tcttttctact	gtagacacta	tcacgagacc	2600
cagattaatt	tctgtggttg	ttacagaata	agtctaataca	aggagaagtt	2650
tctgtttgac	gtttgagtgc	cggctttctg	agtagagtta	ggaaaaccac	2700
gtaacgtagc	atatgatgta	taatagagta	tacccggttac	ttaaaaagaa	2750
gtctgaaatg	ttcgttttgt	ggaaaagaaa	ctagttaaata	ttactattcc	2800
taacccgaat	gaaattagcc	tttgcccttat	tctgtgcatg	ggtaagtaac	2850
ttattttctgc	actgttttgt	tgaactttgt	ggaaacattc	tttcgagttt	2900
gtttttgtca	ttttcgtaac	agtcgtcgaa	ctaggcctca	aaaacatacg	2950
taacgaaaag	gcctagcgag	gcaaattctg	attgatattga	atctatattt	3000
ttctttaaaa	agtcaagggt	tctatattgt	gagtaaatta	aatttacatt	3050
tgagttgttt	gttgctaaga	ggtagtaaat	gtaagagagt	actggttcct	3100
tcagtagtga	gtatttctca	tagtgcagct	ttattttatct	ccaggatgtt	3150
tttgtggctg	tatttgattg	atatgtgctt	cttctgattc	ttgctaattt	3200
ccaaccatat	tgaataaatg	tgatcaagtc	a	3231	

```
<210> 15
<211> 737
<212> PRT
<213> Homo Sapien
```


				110					115					120				
Cys	Ile	Cys	Asn	Glu 125	Gly	Tyr	Glu	Gly	Pro 130	Asn	Cys	Glu	Gln	Ala 135				
Leu	Pro	Ser	Leu	Pro 140	Ala	Thr	Gly	Trp	Thr 145	Glu	Ser	Met	Ala	Pro 150				
Arg	Gln	Leu	Gln	Pro 155	Val	Pro	Ala	Thr	Gln 160	Glu	Pro	Asp	Lys	Ile 165				
Leu	Pro	Arg	Ser	Gln 170	Ala	Thr	Val	Thr	Leu 175	Pro	Thr	Trp	Gln	Pro 180				
Lys	Thr	Gly	Gln	Lys 185	Val	Val	Glu	Met	Lys 190	Trp	Asp	Gln	Val	Glu 195				
Val	Ile	Pro	Asp	Ile 200	Ala	Cys	Gly	Asn	Ala 205	Ser	Ser	Asn	Ser	Ser 210				
Ala	Gly	Gly	Arg	Leu 215	Val	Ser	Phe	Glu	Val 220	Pro	Gln	Asn	Thr	Ser 225				
Val	Lys	Ile	Arg	Gln 230	Asp	Ala	Thr	Ala	Ser 235	Leu	Ile	Leu	Leu	Trp 240				
Lys	Val	Thr	Ala	Thr 245	Gly	Phe	Gln	Gln	Cys 250	Ser	Leu	Ile	Asp	Gly 255				
Arg	Ser	Val	Thr	Pro 260	Leu	Gln	Ala	Ser	Gly 265	Gly	Leu	Val	Leu	Leu 270				
Glu	Glu	Met	Leu	Ala 275	Leu	Gly	Asn	Asn	His 280	Phe	Ile	Gly	Phe	Val 285				
Asn	Asp	Ser	Val	Thr 290	Lys	Ser	Ile	Val	Ala 295	Leu	Arg	Leu	Thr	Leu 300				
Val	Val	Lys	Val	Ser 305	Thr	Cys	Val	Pro	Gly 310	Glu	Ser	His	Ala	Asn 315				
Asp	Leu	Glu	Cys	Ser 320	Gly	Lys	Gly	Lys	Cys 325	Thr	Thr	Lys	Pro	Ser 330				
Glu	Ala	Thr	Phe	Ser 335	Cys	Thr	Cys	Glu	Glu 340	Gln	Tyr	Val	Gly	Thr 345				
Phe	Cys	Glu	Glu	Tyr 350	Asp	Ala	Cys	Gln	Arg 355	Lys	Pro	Cys	Gln	Asn 360				
Asn	Ala	Ser	Cys	Ile 365	Asp	Ala	Asn	Glu	Lys 370	Gln	Asp	Gly	Ser	Asn 375				
Phe	Thr	Cys	Val	Cys 380	Leu	Pro	Gly	Tyr	Thr 385	Gly	Glu	Leu	Cys	Gln 390				
Ser	Lys	Ile	Asp	Tyr 395	Cys	Ile	Leu	Asp	Pro 400	Cys	Arg	Asn	Gly	Ala 405				

09443-03001

Thr Cys Ile Ser	Ser Leu Ser Gly Phe Thr Cys Gln Cys Pro Glu	410	415	420
Gly Tyr Phe Gly	Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala	425	430	435
Ser Ser Pro Cys	Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val	440	445	450
His Phe Thr Cys	Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys	455	460	465
Ala Gln Leu Ile	Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly	470	475	480
Thr Cys Arg Ser	Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro	485	490	495
Gly Tyr His Gly	Leu Tyr Cys Glu Glu Glu Tyr Asn Glu Cys Leu	500	505	510
Ser Ala Pro Cys	Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn	515	520	525
Gly Tyr Glu Cys	Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys	530	535	540
Glu Leu Tyr Lys	Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly	545	550	555
Ala Thr Cys Asp	Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala	560	565	570
Pro Gly Phe Thr	Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys	575	580	585
Asp Ser Asn Pro	Cys His His Gly Gly Ser Cys Leu Asp Gln Pro	590	595	600
Asn Gly Tyr Asn	Cys His Cys Pro His Gly Trp Val Gly Ala Asn	605	610	615
Cys Glu Ile His	Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser	620	625	630
Leu Thr Asn Met	Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala	635	640	645
Leu Cys Val Ala	Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly	650	655	660
Ile Cys Arg Ile	Ser Arg Ile Glu Tyr Gln Gly Ser Ser Arg Pro	665	670	675
Ala Tyr Glu Glu	Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe	680	685	690
Ser Asn Ala Ile	Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys			

TOEBO"2ETH660

695	700	705
Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp		
710	715	720
Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys		
725	730	735

Asp Leu

<210> 16
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 16
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 17
 caggaaacag ctatgaccac ctgcacacct gcaaatecat t 41

<210> 18
 <211> 508
 <212> DNA
 <213> Homo Sapien

<400> 18
 ctctggaagg tcacggccac aggattccaa cagtgtctcc tcatagatgg 50
 acgaaagtgt gacccccctt tcaggctttc agggggactg gtcctcctgg 100
 aggagatgct cgccttgggg aataatcact ttattgggtt tgtgaatgat 150
 tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200
 cagcacctgt gtgcggggg agagtcacgc aatgacttg gagggttcag 250
 gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300
 tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
 gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
 aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450
 ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19
<211> 508
<212> DNA
<213> Homo Sapien

<400> 19
ctctggaagg tcacggccac aggattccaa cagtgtctccc tcatagatgg 50
acgaaagtgt gacccccctt tcaggctttc aggggggactg gtcctcctgg 100
aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150
tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggggaaggt 200
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250
gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
aagatgggag caatttcacc tgtgtttgcc ttcttggtta tactggagag 450
ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500
taggggag 508

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 20
ctctggaagg tcacggccac agg 23

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
ctcagttcgg ttggcaaagc tctc 24

<210> 22
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

[illegible]

gctttgccaa ccgaactga 69

<213> Homo Sapien

agcttcaggg tgctcttcgt qqaaacctgc tgcqggtctt cagacaagtq 1150

gaaaagggtac aggaagaaaa caaatggcaa agcccccttgg aggacaagtt 1200
 cccggatgag cagctgagca gttcctgcc ctcgacctc tcacgtctgc 1250
 gtcagagaca gagtctgact tcaggccagg aactcactga gattcccata 1300
 cactggacag ccaagttacc agccaagtgg tcagtctcag agtcctcccc 1350
 ccacatggcc ccagtccttg cagttgtggc caccttccca gtccttattc 1400
 tgtggctctg atgaccacgt tagtcctgcc agatgtcact gtagcaagcc 1450
 acagacaccc cacaagttc ccctgttgtg caggcacaaa tatttctga 1500
 aataaatggt ttggacatag 1520

<210> 24
 <211> 433
 <212> PRT
 <213> Homo Sapien

<400> 24
 Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
 1 5 10 15
 Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
 20 25 30
 Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
 35 40 45
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser
 50 55 60
 Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
 65 70 75
 Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
 80 85 90
 Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
 95 100 105
 Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
 110 115 120
 Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
 125 130 135
 Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
 140 145 150
 Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
 155 160 165
 Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
 170 175 180

00000-2244660

100E90" 2244660

Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala	
				185					190					195	
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser	
				200					205					210	
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	
				215					220					225	
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg	
				230					235					240	
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	
				245					250					255	
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro	
				260					265					270	
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys	
				275					280					285	
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp	
				290					295					300	
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	
				305					310					315	
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu	
				320					325					330	
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	
				335					340					345	
Gln	Val	Glu	Lys	Val	Gln	Glu	Glu	Asn	Lys	Trp	Gln	Ser	Pro	Leu	
				350					355					360	
Glu	Asp	Lys	Phe	Pro	Asp	Glu	Gln	Leu	Ser	Ser	Ser	Cys	His	Ser	
				365					370					375	
Asp	Leu	Ser	Arg	Leu	Arg	Gln	Arg	Gln	Ser	Leu	Thr	Ser	Gly	Gln	
				380					385					390	
Glu	Leu	Thr	Glu	Ile	Pro	Ile	His	Trp	Thr	Ala	Lys	Leu	Pro	Ala	
				395					400					405	
Lys	Trp	Ser	Val	Ser	Glu	Ser	Ser	Pro	His	Met	Ala	Pro	Val	Leu	
				410					415					420	
Ala	Val	Val	Ala	Thr	Phe	Pro	Val	Leu	Ile	Leu	Trp	Leu			
				425					430						

<210> 25
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 25
agttctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtgatggcg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat ccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gagcagattg acctcatagc ccgatgtgt gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
aaaacctata aatattccgg attattcata ccgtcccacc atcgggcgcg 50
gatccgcggc cgcgaattct aaaccaacat gccgggcacc tacgctccct 100
cgaccacact cagtagtccc agcaccagg gcctgcaaga gcaggcacgg 150
gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200
ggtcctaagg cagggtttacc agaaagggt acaggatgtt aacctgcgca 250
atttcagcta cgccagacc agcctggaca ggcttagaga tggcctcgtg 300
ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350
tgccctgcgc ctcacctgg agcagattga cctcatagc ccgatgtgtg 400

09044433-0830001

cctcctattc tgagctggag cttgtgacct cggctaaagc tctgaacgac 450
 actcagaaat tggcctgect catcgggtga gaggggtggcc actcgctgga 500
 caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550
 tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaag 600
 ggcgtccact ccttctacaa caacatcagc gggctgactg actttggtga 650
 gaagggtggtg gcagaaatga accgcctggg catgatggta gacttatccc 700
 atgtctcaga tgctgtggca cggcggggccc tggaagtgtc acaggcacct 750
 gtgatcttct cccactcggc tgcccgggggt gtgtgcaaca gtgctcgga 800
 tgttcttgat gacatcctgc agcttctgaa gaagaacggg ggcgtcgtga 850
 tgggtgtcttt gtccatggga gtaatacagt gcaaccatc agccaatgtg 900
 tccactgtgg cagatcactt cgaccacatc aaggctgtca ttggatccaa 950
 gttcatcggg attggtggag attatgatgg ggccggcaaa ttccctcagg 1000
 ggctggaaga cgtgtccaca taccgggtcc tgatagagga gttgctgagt 1050
 cgtggctgga gtgaggaaga gcttcagggt gtccttcgtg gaaacctgct 1100
 gcgggtcttc agacaagtgg aaaaggtaca ggaagaaaac aaatggcaaa 1150
 gccccttgga ggacaagttc ccggatgagc agctgagcag ttctgccac 1200
 tccgacctct cacgtctgcg tcagagacag agtctgactt caggccagga 1250
 actcactgag attcccatac actggacagc caagttacca gccaaagtgt 1300
 cagtctcaga gtctccccc caccctgaca aaactcacac atgccaccg 1350
 tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttccccc 1400
 aaaacccaag gacacc 1416

<210> 30
 <211> 446
 <212> PRT
 <213> Homo Sapien

<400> 30
 Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
 1 5 10 15
 Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
 20 25 30
 Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
 35 40 45
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

FOOEEBO" 2E444660

	50		55		60
Tyr Gly Gln Thr Ser	Leu Asp Arg Leu Arg Asp Gly Leu Val Gly				
	65		70		75
Ala Gln Phe Trp Ser	Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg				
	80		85		90
Asp Ala Leu Arg Leu	Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg				
	95		100		105
Met Cys Ala Ser Tyr	Ser Glu Leu Glu Leu Val Thr Ser Ala Lys				
	110		115		120
Ala Leu Asn Asp Thr	Gln Lys Leu Ala Cys Leu Ile Gly Val Glu				
	125		130		135
Gly Gly His Ser Leu	Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe				
	140		145		150
Tyr Met Leu Gly Val	Arg Tyr Leu Thr Leu Thr His Thr Cys Asn				
	155		160		165
Thr Pro Trp Ala Glu	Ser Ser Ala Lys Gly Val His Ser Phe Tyr				
	170		175		180
Asn Asn Ile Ser Gly	Leu Thr Asp Phe Gly Glu Lys Val Val Ala				
	185		190		195
Glu Met Asn Arg Leu	Gly Met Met Val Asp Leu Ser His Val Ser				
	200		205		210
Asp Ala Val Ala Arg	Arg Ala Leu Glu Val Ser Gln Ala Pro Val				
	215		220		225
Ile Phe Ser His Ser	Ala Ala Arg Gly Val Cys Asn Ser Ala Arg				
	230		235		240
Asn Val Pro Asp Asp	Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly				
	245		250		255
Val Val Met Val Ser	Leu Ser Met Gly Val Ile Gln Cys Asn Pro				
	260		265		270
Ser Ala Asn Val Ser	Thr Val Ala Asp His Phe Asp His Ile Lys				
	275		280		285
Ala Val Ile Gly Ser	Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp				
	290		295		300
Gly Ala Gly Lys Phe	Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr				
	305		310		315
Pro Val Leu Ile Glu	Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu				
	320		325		330
Glu Leu Gln Gly Val	Leu Arg Gly Asn Leu Leu Arg Val Phe Arg				
	335		340		345

atatcctctgga	tgtggtgacc	acggaccccc	cgccccgacgt	gcacgtgagc	850
cgcgctcgggg	gcctggagga	ccagctgagc	gtgcgctggg	tgtcgccacc	900
cgccctcaag	gatttcctct	ttcaagccaa	ataccagatc	cgctaccgag	950
tggaggacag	tgtggactgg	aagggtggtg	acgatgtgag	caaccagacc	1000
tcctgccgcc	tggccggcct	gaaacccggc	accgtgtact	tcgtgcaagt	1050
gcgctgcaac	ccctttggca	tctatggctc	caagaaagcc	gggatctgga	1100
gtgagtggag	ccacccaca	gccgcctcca	ctccccgcag	tgagcgcccg	1150
ggccccggcg	gcggggcgctg	cgaaccgcgg	ggcggagagc	cgagctcggg	1200
gccggtgcgg	cgcgagctca	agcagttcct	gggctggctc	aagaagcacg	1250
cgtactgctc	caacctcagc	ttccgcctct	acgaccagtg	gcgagcctgg	1300
atgcagaagt	cgcacaagac	ccgcaaccag	gacgagggga	tcctgccctc	1350
gggcagacgg	ggcacggcga	gaggtcctgc	cagataagct	gtaggggctc	1400
aggccaccct	ccctgccacg	tggagacgca	gaggccgaac	ccaaactggg	1450
gccacctctg	tacctcact	tcagggcacc	tgagccaccc	tcagcaggag	1500
ctggggtggc	ccctgagctc	caacggccat	aacagctctg	actcccacgt	1550
gaggccacct	ttgggtgcac	cccagtgggt	gtgtgtgtgt	gtgtgagggg	1600
tggttgagtt	gcctagaacc	cctgccaggg	ctgggggtga	gaaggggagt	1650
cattactccc	cattacctag	ggccccctcca	aaagagtctt	tttaaataaa	1700
tgagctattt	aggtgctgtg	attgtgaaaa	aaaaaaaaaa	aaaaaaaaaa	1750
aaaaaaaaaa	aaaaaaaaaa	aaaaacaaaa	aaaaaaaaaa	1790	

```
<210> 32
<211> 422
<212> PRT
<213> Homo Sapien
```

Ser	Val	His	Gly	Asp 65	Pro	Pro	Gly	Ala	Thr 70	Ala	Glu	Gly	Leu	Tyr 75
Trp	Thr	Leu	Asn	Gly 80	Arg	Arg	Leu	Pro	Pro 85	Glu	Leu	Ser	Arg	Val 90
Leu	Asn	Ala	Ser	Thr 95	Leu	Ala	Leu	Ala	Leu 100	Ala	Asn	Leu	Asn	Gly 105
Ser	Arg	Gln	Arg	Ser 110	Gly	Asp	Asn	Leu	Val 115	Cys	His	Ala	Arg	Asp 120
Gly	Ser	Ile	Leu	Ala 125	Gly	Ser	Cys	Leu	Tyr 130	Val	Gly	Leu	Pro	Pro 135
Glu	Lys	Pro	Val	Asn 140	Ile	Ser	Cys	Trp	Ser 145	Lys	Asn	Met	Lys	Asp 150
Leu	Thr	Cys	Arg	Trp 155	Thr	Pro	Gly	Ala	His 160	Gly	Glu	Thr	Phe	Leu 165
His	Thr	Asn	Tyr	Ser 170	Leu	Lys	Tyr	Lys	Leu 175	Arg	Trp	Tyr	Gly	Gln 180
Asp	Asn	Thr	Cys	Glu 185	Glu	Tyr	His	Thr	Val 190	Gly	Pro	His	Ser	Cys 195
His	Ile	Pro	Lys	Asp 200	Leu	Ala	Leu	Phe	Thr 205	Pro	Tyr	Glu	Ile	Trp 210
Val	Glu	Ala	Thr	Asn 215	Arg	Leu	Gly	Ser	Ala 220	Arg	Ser	Asp	Val	Leu 225
Thr	Leu	Asp	Ile	Leu 230	Asp	Val	Val	Thr	Thr 235	Asp	Pro	Pro	Pro	Asp 240
Val	His	Val	Ser	Arg 245	Val	Gly	Gly	Leu	Glu 250	Asp	Gln	Leu	Ser	Val 255
Arg	Trp	Val	Ser	Pro 260	Pro	Ala	Leu	Lys	Asp 265	Phe	Leu	Phe	Gln	Ala 270
Lys	Tyr	Gln	Ile	Arg 275	Tyr	Arg	Val	Glu	Asp 280	Ser	Val	Asp	Trp	Lys 285
Val	Val	Asp	Asp	Val 290	Ser	Asn	Gln	Thr	Ser 295	Cys	Arg	Leu	Ala	Gly 300
Leu	Lys	Pro	Gly	Thr 305	Val	Tyr	Phe	Val	Gln 310	Val	Arg	Cys	Asn	Pro 315
Phe	Gly	Ile	Tyr	Gly 320	Ser	Lys	Lys	Ala	Gly 325	Ile	Trp	Ser	Glu	Trp 330
Ser	His	Pro	Thr	Ala 335	Ala	Ser	Thr	Pro	Arg 340	Ser	Glu	Arg	Pro	Gly 345
Pro	Gly	Gly	Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser

350	355	360
Gly Pro Val Arg	Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys	
365	370	375
Lys His Ala Tyr	Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln	
380	385	390
Trp Arg Ala Trp	Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp	
395	400	405
Glu Gly Ile Leu	Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro	
410	415	420
Ala Arg		

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 33
 cccgcccgac gtgcacgtga gcc 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
 tgagccagcc caggaactgc ttg 23

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 35
 caagtgcgct gcaacccctt tggcatctat ggctccaaga aagccgggat 50

<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

<400> 36
 cccacgcgctc cgctggtggtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg 100
 atgaaatttc ttctggacat cctcctgctt ctcccgttac tgatcgtctg 150
 ctccctagag tcttctgtga agctttttat tctaagagg agaaaatcag 200
 tcaccggcga aatcgtgctg attacaggag ctgggcatgg aattgggaga 250
 ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
 tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350
 gtgccaaagg tcataccttt gtggtagact gcagcaaccg agaagatatt 400
 tacagctctg caaagaagggt gaaggcagaa attggagatg ttagtatttt 450
 agtaaataat gctgggtgtag tctatacatc agatttggtt gctacacaag 500
 atcctcagat tgaaaagact tttgaagtta atgtacttgc acatttctgg 550
 actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
 tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg 650
 cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 700
 gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg 750
 tctaatttc gtaaacactg gcttcatcaa aaatccaagt acaagtttgg 800
 gaccactctt ggaacctgag gaagtggtaa acaggctgat gcatgggatt 850
 ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
 aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa 950
 aaatcagtgt taagtttgat gcagttattg gatataaaat gaaagcgcaa 1000
 taagcaccta gttttctgaa aactgattta ccaggtttag gttgatgtca 1050
 tctaatagtg ccagaatttt aatgtttgaa cttctgtttt ttctaattat 1100
 ccccatctt tcaatatcat ttttgaggct ttggcagctc tcatttacta 1150
 ccacttgctc tttagccaaa agctgattac atatgatata aacagagaaa 1200
 tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac 1250
 tttattaaaa taatttccaa gattatttgt ggctcacctg aaggctttgc 1300
 aaaatttgta ccataaccgt ttattttaaca tataattttta tttttgattg 1350
 cacttaaatt ttgtataatt tgtgtttctt tttctgttct acataaaatc 1400
 agaaacttca agctctctaa ataaaatgaa ggactatata tagtggattt 1450
 tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccattt 1500

200										205					210				
Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn		Phe	Val	Asn	Thr	Gly	Phe				
215										220					225				
Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly		Pro	Thr	Leu	Glu	Pro	Glu				
230										235					240				
Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly		Ile	Leu	Thr	Glu	Gln	Lys				
245										250					255				
Met	Ile	Phe	Ile	Pro	Ser	Ser	Ile	Ala		Phe	Leu	Thr	Thr	Leu	Glu				
260										265					270				
Arg	Ile	Leu	Pro	Glu	Arg	Phe	Leu	Ala		Val	Leu	Lys	Arg	Lys	Ile				
275										280					285				
Ser	Val	Lys	Phe	Asp	Ala	Val	Ile	Gly		Tyr	Lys	Met	Lys	Ala	Gln				
290										295					300				

<400> 41

gactagttct cttggagtct gggaggagga aagcggagcc ggcagggagc 50
 gaaccaggac tggggtgacg gcagggcagg gggcgccctgg ccggggagaa 100
 gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150
 ccgaaggagg ccatcgggga gccgggaggg gggactgcga gaggaccccg 200
 gcgtccgggc tcccgggtgc agcgctatga ggccactcct cgtcctgctg 250
 ctctggggcc tggcgggcgg ctcgccccc ctggacgaca acaagatccc 300
 cagcctctgc ccggggcacc ccggccttcc aggcacgccc ggccaccatg 350
 gcagccaggg cttgccgggc cgcgatggcc gcgacggccg cgacggcgcg 400
 cccggggctc cgggagagaa aggcgagggc gggaggccgg gactgccggg 450
 acctcgaggg gaccccgggc cgcgaggaga ggcgggaccc gcggggccca 500
 ccgggcctgc cggggagtgc tcgggtgcct cgcgatccgc cttcagcgcc 550
 aagcgctccg agagccgggt gcctccgccg tctgacgcac ctttgcctt 600
 cgaccgcgtg ctggtgaacg agcagggaca ttacgacgcc gtcaccggca 650
 agttcacctg ccaggtgcct ggggtctact acttcgccgt ccatgccacc 700
 gtctaccggg ccagcctgca gtttgatctg gtgaagaatg gcgaatccat 750
 tgcctcttcc ttccagtttt tcgggggggtg gccaagcca gcctcgctct 800
 cggggggggc catggtgagg ctggagcctg aggaccaagt gtgggtgcag 850
 gtgggtgtgg gtgactacat tggcatctat gccagcatca agacagacag 900
 caccttctcc ggatttctgg tgtactccga ctggcacagc tccccagtct 950
 ttgcttagtg cccactgcaa agtgagctca tgctctcact cctagaagga 1000
 ggggtgtgagg ctgacaacca ggtcatccag gagggtctggc ccccttgaa 1050
 tattgtgaat gactaggag gtggggtaga gcactctccg tcctgctgct 1100
 ggcaaggaat gggaacagtg gctgtctgcg atcaggtctg gcagcatggg 1150
 gcagtggctg gatttctgcc caagaccaga ggagtgtgct gtgctggcaa 1200
 gtgtaagtcc ccagttgct ctggtccagg agcccacggg ggggtgctct 1250
 ctctctggtc ctctgcttct ctggatctc cccacccct cctgctcctg 1300
 gggccggccc ttttctcaga gatcactcaa taaacctag aaccctcata 1350
 aaaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243
 <212> PRT
 <213> Homo Sapien

<400> 42

Met	Arg	Pro	Leu	Leu	Val	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Gly
1				5					10					15
Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly
				20					25					30
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly
				35					40					45
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly
				50					55					60
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly
				65					70					75
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly
				80					85					90
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala
				95					100					105
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp
				110					115					120
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His
				125					130					135
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val
				140					145					150
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln
				155					160					165
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln
				170					175					180
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala
				185					190					195
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly
				200					205					210
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser
				215					220					225
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro
				230					235					240

Val Phe Ala

<210> 43
 <211> 24

FOOESD" EETHH660

[illegible]

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
acctgacggg cccaacagac ccatgctgca tccagagacc tcccctggcc 150
gggggcatct cctggctgtg ctctggccc tccttggcac cacctgggca 200
gaggtgtggc caccacagct gcaggagcag gctccgatgg cggagccct 250
gaacaggaag gagagtttct tgctcctctc cctgcacaac cgctgcgca 300
gctgggtcca gcccctgcg gctgacatgc ggaggctgga ctggagtgc 350
agcctggccc aactggctca agccaggga gccctctgtg gaatcccaac 400
cccagacctg gcatccggcc tgtggcgcac cctgcaagtg ggctggaaca 450
tgcagctgct gcccgcgggc ttggcgctct ttgttgaagt ggtcagccta 500
tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550
caacgccacc tgcaccact acacgcagct cgtgtgggccc acctcaagcc 600
agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650
gcctttgtct gtgcctactc ccccggaggc aactgggagg tcaacgggaa 700
gacaatcatc ccctataaga aggggtgcctg gtgttcgctc tgcacagcca 750
gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800
gtccccagga atcctgtgct catgagctgc cagaaccatg gacgtctcaa 850
catcagcacc tgccactgcc actgtccccc tggctacacg ggcagatact 900
gccaagtgcg gtgcagcctg cagtgtgtgc acggccgggt cgggaggag 950
gagtgtcgt gcgtctgtga catcggtac gggggagccc agtgtgccac 1000
caagggtgat tttcccttcc acacctgtga cctgaggatc gacggagact 1050
gcttcatggt gtcttcagag gcagacacct attacagagc caggatgaaa 1100
tgtcagagga aaggcggggg gctggccag atcaagagcc agaaagtgc 1150

ggacatcctc gccttctatc tgggcccgcct ggagaccacc aacgaggtga 1200
 ctgacagtga cttcgagacc aggaacttct ggatcgggct cacctacaag 1250
 accgccaagg actccttccg ctggggccaca ggggagcacc aggccttcac 1300
 cagttttgcc tttgggcagc ctgacaacca cgggctggtg tggctgagtg 1350
 ctgccatggg gtttggcaac tgcgtggagc tgcaggcttc agctgccttc 1400
 aactggaacg accagcgtg caaaacccga aaccgttaca tctgccagtt 1450
 tgcccaggag cacatctccc ggtggggccc agggctctga ggcctgacca 1500
 catggctccc tgcctgccc tgggagcacc ggctctgctt acctgtctgc 1550
 ccacctgtct ggaacaaggg ccaggttaag accacatgcc tcatgtccaa 1600
 agaggtctca gaccttgac aatgccagaa gttgggcaga gagaggcagg 1650
 gaggccagtg agggccaggg agtgagtgtt agaagaagct ggggcccttc 1700
 gcctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750
 acaccgccag tggtcacaaa aggctgctct cttccacctg gccagaccc 1800
 tgtggggcag cggagcttcc ctgtggcatg aacccacgg ggtattaaat 1850
 tatgaatcag ctgaaaaaaaa aaaaaa 1876

<210> 50
 <211> 455
 <212> PRT
 <213> Homo Sapien

<400> 50
 Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala
 1 5 10 15
 Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
 20 25 30
 Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
 35 40 45
 Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser
 50 55 60
 Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
 65 70 75
 Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
 80 85 90
 Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
 95 100 105
 Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

					110					115					120
Val	Glu	Val	Val	Ser	Leu	Trp	Phe	Ala	Glu	Gly	Gln	Arg	Tyr	Ser	
				125					130					135	
His	Ala	Ala	Gly	Glu	Cys	Ala	Arg	Asn	Ala	Thr	Cys	Thr	His	Tyr	
				140					145					150	
Thr	Gln	Leu	Val	Trp	Ala	Thr	Ser	Ser	Gln	Leu	Gly	Cys	Gly	Arg	
				155					160					165	
His	Leu	Cys	Ser	Ala	Gly	Gln	Thr	Ala	Ile	Glu	Ala	Phe	Val	Cys	
				170					175					180	
Ala	Tyr	Ser	Pro	Gly	Gly	Asn	Trp	Glu	Val	Asn	Gly	Lys	Thr	Ile	
				185					190					195	
Ile	Pro	Tyr	Lys	Lys	Gly	Ala	Trp	Cys	Ser	Leu	Cys	Thr	Ala	Ser	
				200					205					210	
Val	Ser	Gly	Cys	Phe	Lys	Ala	Trp	Asp	His	Ala	Gly	Gly	Leu	Cys	
				215					220					225	
Glu	Val	Pro	Arg	Asn	Pro	Cys	Arg	Met	Ser	Cys	Gln	Asn	His	Gly	
				230					235					240	
Arg	Leu	Asn	Ile	Ser	Thr	Cys	His	Cys	His	Cys	Pro	Pro	Gly	Tyr	
				245					250					255	
Thr	Gly	Arg	Tyr	Cys	Gln	Val	Arg	Cys	Ser	Leu	Gln	Cys	Val	His	
				260					265					270	
Gly	Arg	Phe	Arg	Glu	Glu	Glu	Cys	Ser	Cys	Val	Cys	Asp	Ile	Gly	
				275					280					285	
Tyr	Gly	Gly	Ala	Gln	Cys	Ala	Thr	Lys	Val	His	Phe	Pro	Phe	His	
				290					295					300	
Thr	Cys	Asp	Leu	Arg	Ile	Asp	Gly	Asp	Cys	Phe	Met	Val	Ser	Ser	
				305					310					315	
Glu	Ala	Asp	Thr	Tyr	Tyr	Arg	Ala	Arg	Met	Lys	Cys	Gln	Arg	Lys	
				320					325					330	
Gly	Gly	Val	Leu	Ala	Gln	Ile	Lys	Ser	Gln	Lys	Val	Gln	Asp	Ile	
				335					340					345	
Leu	Ala	Phe	Tyr	Leu	Gly	Arg	Leu	Glu	Thr	Thr	Asn	Glu	Val	Thr	
				350					355					360	
Asp	Ser	Asp	Phe	Glu	Thr	Arg	Asn	Phe	Trp	Ile	Gly	Leu	Thr	Tyr	
				365					370					375	
Lys	Thr	Ala	Lys	Asp	Ser	Phe	Arg	Trp	Ala	Thr	Gly	Glu	His	Gln	
				380					385					390	
Ala	Phe	Thr	Ser	Phe	Ala	Phe	Gly	Gln	Pro	Asp	Asn	His	Gly	Leu	
				395					400					405	

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
 410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
 425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
 440 445 450

Trp Gly Pro Gly Ser
 455

<210> 51
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 51
 aggaacttct ggatcgggct cacc 24

<210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 52
 gggctctgggc caggtggaag agag 24

<210> 53
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 gccaaaggact ccttcgctg ggccacagg gagcaccagg ccttc 45

<210> 54
 <211> 2331
 <212> DNA
 <213> Homo Sapien

<400> 54
 cggacgcgtg ggctgggagc tgcaaagcgt gtcccgcagg gtcccgcagg 50
 gtcccgcagg ctgccccgc catgctcctg ctgctggggc tgtgcctggg 100
 gctgtccctg tgtgtggggc cgcaggaaga ggcgcagagc tggggccact 150
 cttcgagca ggatggactc aggggtccga ggcaagtcag actgttgag 200

aggctgaaaa	ccaaaccttt	gatgacagaa	ttctcagtga	agtctaccat	250
catttcccgt	tatgccttca	ctacggtttc	ctgcagaatg	ctgaacagag	300
cttctgaaga	ccaggacatt	gagttccaga	tgcagattcc	agctgcagct	350
ttcatcacca	acttcactat	gcttattgga	gacaagggtg	atcagggcga	400
aattacagag	agagaaaaga	agagtgggtg	tagggtaaaa	gagaaaagga	450
ataaaaccac	agaagaaaat	ggagagaagg	ggactgaaat	attcagagct	500
tctgcagtga	ttcccagcaa	ggacaaagcc	gcctttttcc	tgagttatga	550
ggagcttctg	cagaggcgcc	tgggcaagta	cgagcacagc	atcagcgtgc	600
ggccccagca	gctgtccggg	aggctgagcg	tggacgtgaa	tatcctggag	650
agcgcgggca	tgcctccctt	ggaggtgctg	ccgcttcaca	acagcaggca	700
gaggggagct	gggcgcgggg	aagatgattc	tgggcctccc	ccatctactg	750
tcattaacca	aaatgaaaca	tttgccaaca	taatttttaa	acctactgta	800
gtacaacaag	ccaggattgc	ccagaatgga	attttgggag	actttatcat	850
tagatatgac	gtcaatagag	aacagagcat	tggggacatc	caggttctaa	900
atggctattt	tgtgcactac	tttgctccta	aagaccttcc	tcctttaccc	950
aagaatgtgg	tattcgtgct	tgacagcagt	gcttctatgg	tgggaaccaa	1000
actccggcag	accaaggatg	ccctcttcac	aattctccat	gacctccgac	1050
cccaggaccg	tttcagtatc	attggatttt	ccaaccggat	caaagtatgg	1100
aaggaccact	tgatatcagt	cactccagac	agcatcaggg	atgggaaagt	1150
gtacattcac	catatgtcac	ccactggagg	cacagacatc	aacggggccc	1200
tgcagagggc	catcaggctc	ctcaacaagt	acgtggccca	cagtggcatt	1250
ggagaccgga	gcgtgtccct	catcgtcttc	ctgacggatg	ggaagcccac	1300
ggtcggggag	acgcacaccc	tcaagatcct	caacaacacc	cgagaggccg	1350
cccagggcc	agtctgcac	ttcaccattg	gcacgggcaa	cgacgtggac	1400
ttcaggctgc	tggagaaact	gtcgtgggag	aactgtggcc	tcacacggcg	1450
cgtgcacgag	gaggaggacg	caggctcgca	gctcatcggg	ttctacgatg	1500
aaatcaggac	ccgctcctc	tctgacatcc	gcacgatta	tccccccagc	1550
tcagtgggtg	aggccaccaa	gacctgttc	cccaactact	tcaacggctc	1600
ggagatcatc	attgcgggga	agctgggtga	caggaagctg	gatcacctgc	1650

acgtggaggt caccgccagc aacagtaaga aattcatcat cctgaagaca 1700
 gatgtgcctg tgcggcctca gaaggcaggg aaagatgtca caggaagccc 1750
 caggcctgga ggcgatggag agggggacac caaccacatc gagcgtctct 1800
 ggagctacct caccacaaag gagctgctga gctcctggct gcaaagtga 1850
 gatgaaccgg agaaggagcg gctgcgccag cgggcccagg cctgggctgt 1900
 gagctaccgc ttctcactc ccttcacctc catgaagctg agggggccgg 1950
 tcccacgcat ggatggcctg gaggaggccc acggcatgtc ggctgccatg 2000
 ggacccgaac cgggtggtgca gagcgtgcga ggagctggca cgcagccagg 2050
 acctttgctc aagaagccaa actccgtcaa aaaaaaacia aacaaaacia 2100
 aaaaaagaca tgggagagat ggtgtttttc ctctccacca cctggggata 2150
 cgatgagaag atggccacct gcaagccagg aagacggccc tcaccagaca 2200
 ccatgtctgc tggcaccttg atcttgacc tccagcctc cagaactgtg 2250
 agaaataaat gtgttttgtt taagctaaaa aaaaaaaaaa aaaaaaaaaa 2300
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2331

<210> 55
 <211> 694
 <212> PRT
 <213> Homo Sapien

<400> 55
 Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val
 1 5 10 15
 Gly Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln
 20 25 30
 Asp Gly Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu
 35 40 45
 Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile
 50 55 60
 Ile Ser Arg Tyr Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn
 65 70 75
 Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro
 80 85 90
 Ala Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys
 95 100 105
 Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp
 110 115 120

Arg	Val	Lys	Glu	Lys	Arg	Asn	Lys	Thr	Thr	Glu	Glu	Asn	Gly	Glu		125	130	135
Lys	Gly	Thr	Glu	Ile	Phe	Arg	Ala	Ser	Ala	Val	Ile	Pro	Ser	Lys		140	145	150
Asp	Lys	Ala	Ala	Phe	Phe	Leu	Ser	Tyr	Glu	Glu	Leu	Leu	Gln	Arg		155	160	165
Arg	Leu	Gly	Lys	Tyr	Glu	His	Ser	Ile	Ser	Val	Arg	Pro	Gln	Gln		170	175	180
Leu	Ser	Gly	Arg	Leu	Ser	Val	Asp	Val	Asn	Ile	Leu	Glu	Ser	Ala		185	190	195
Gly	Ile	Ala	Ser	Leu	Glu	Val	Leu	Pro	Leu	His	Asn	Ser	Arg	Gln		200	205	210
Arg	Gly	Ser	Gly	Arg	Gly	Glu	Asp	Asp	Ser	Gly	Pro	Pro	Pro	Ser		215	220	225
Thr	Val	Ile	Asn	Gln	Asn	Glu	Thr	Phe	Ala	Asn	Ile	Ile	Phe	Lys		230	235	240
Pro	Thr	Val	Val	Gln	Gln	Ala	Arg	Ile	Ala	Gln	Asn	Gly	Ile	Leu		245	250	255
Gly	Asp	Phe	Ile	Ile	Arg	Tyr	Asp	Val	Asn	Arg	Glu	Gln	Ser	Ile		260	265	270
Gly	Asp	Ile	Gln	Val	Leu	Asn	Gly	Tyr	Phe	Val	His	Tyr	Phe	Ala		275	280	285
Pro	Lys	Asp	Leu	Pro	Pro	Leu	Pro	Lys	Asn	Val	Val	Phe	Val	Leu		290	295	300
Asp	Ser	Ser	Ala	Ser	Met	Val	Gly	Thr	Lys	Leu	Arg	Gln	Thr	Lys		305	310	315
Asp	Ala	Leu	Phe	Thr	Ile	Leu	His	Asp	Leu	Arg	Pro	Gln	Asp	Arg		320	325	330
Phe	Ser	Ile	Ile	Gly	Phe	Ser	Asn	Arg	Ile	Lys	Val	Trp	Lys	Asp		335	340	345
His	Leu	Ile	Ser	Val	Thr	Pro	Asp	Ser	Ile	Arg	Asp	Gly	Lys	Val		350	355	360
Tyr	Ile	His	His	Met	Ser	Pro	Thr	Gly	Gly	Thr	Asp	Ile	Asn	Gly		365	370	375
Ala	Leu	Gln	Arg	Ala	Ile	Arg	Leu	Leu	Asn	Lys	Tyr	Val	Ala	His		380	385	390
Ser	Gly	Ile	Gly	Asp	Arg	Ser	Val	Ser	Leu	Ile	Val	Phe	Leu	Thr		395	400	405
Asp	Gly	Lys	Pro	Thr	Val	Gly	Glu	Thr	His	Thr	Leu	Lys	Ile	Leu				

410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr		
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu		
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu		
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		
575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		
620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		
680	685	690
Leu Gly Ile Arg		

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatata agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
cggacgcgtg ggggtgcccga catggcgagt gtagtgctgc cgagcggatc 50
ccagtgtgctg gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100
tgctgttgct cttctccgcc gcggcactga tccccacagg tgatgggcag 150
aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgaccat 200

Ala	Ala	Ala	Ala	Ala 20	Pro	Pro	Gly	Leu	Arg 25	Leu	Leu	Leu	Leu	Leu 30
Phe	Ser	Ala	Ala	Ala 35	Leu	Ile	Pro	Thr	Gly 40	Asp	Gly	Gln	Asn	Leu 45
Phe	Thr	Lys	Asp	Val 50	Thr	Val	Ile	Glu	Gly 55	Glu	Val	Ala	Thr	Ile 60
Ser	Cys	Gln	Val	Asn 65	Lys	Ser	Asp	Asp	Ser 70	Val	Ile	Gln	Leu	Leu 75
Asn	Pro	Asn	Arg	Gln 80	Thr	Ile	Tyr	Phe	Arg 85	Asp	Phe	Arg	Pro	Leu 90
Lys	Asp	Ser	Arg	Phe 95	Gln	Leu	Leu	Asn	Phe 100	Ser	Ser	Ser	Glu	Leu 105
Lys	Val	Ser	Leu	Thr 110	Asn	Val	Ser	Ile	Ser 115	Asp	Glu	Gly	Arg	Tyr 120
Phe	Cys	Gln	Leu	Tyr 125	Thr	Asp	Pro	Pro	Gln 130	Glu	Ser	Tyr	Thr	Thr 135
Ile	Thr	Val	Leu	Val 140	Pro	Pro	Arg	Asn	Leu 145	Met	Ile	Asp	Ile	Gln 150
Lys	Asp	Thr	Ala	Val 155	Glu	Gly	Glu	Glu	Ile 160	Glu	Val	Asn	Cys	Thr 165
Ala	Met	Ala	Ser	Lys 170	Pro	Ala	Thr	Thr	Ile 175	Arg	Trp	Phe	Lys	Gly 180
Asn	Thr	Glu	Leu	Lys 185	Gly	Lys	Ser	Glu	Val 190	Glu	Glu	Trp	Ser	Asp 195
Met	Tyr	Thr	Val	Thr 200	Ser	Gln	Leu	Met	Leu 205	Lys	Val	His	Lys	Glu 210
Asp	Asp	Gly	Val	Pro 215	Val	Ile	Cys	Gln	Val 220	Glu	His	Pro	Ala	Val 225
Thr	Gly	Asn	Leu	Gln 230	Thr	Gln	Arg	Tyr	Leu 235	Glu	Val	Gln	Tyr	Lys 240
Pro	Gln	Val	His	Ile 245	Gln	Met	Thr	Tyr	Pro 250	Leu	Gln	Gly	Leu	Thr 255
Arg	Glu	Gly	Asp	Ala 260	Leu	Glu	Leu	Thr	Cys 265	Glu	Ala	Ile	Gly	Lys 270
Pro	Gln	Pro	Val	Met 275	Val	Thr	Trp	Val	Arg 280	Val	Asp	Asp	Glu	Met 285
Pro	Gln	His	Ala	Val 290	Leu	Ser	Gly	Pro	Asn 295	Leu	Phe	Ile	Asn	Asn 300
Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn

	305		310		315
Ile Val Gly Lys	Ala His Ser Asp Tyr	Met Leu Tyr Val Tyr	Asp		
	320	325	330		
Pro Pro Thr Thr	Ile Pro Pro Pro Thr	Thr Thr Thr Thr Thr	Thr		
	335	340	345		
Thr Thr Thr Thr	Thr Thr Ile Leu Thr	Ile Ile Thr Asp Ser	Arg		
	350	355	360		
Ala Gly Glu Glu	Gly Ser Ile Arg Ala	Val Asp His Ala Val	Ile		
	365	370	375		
Gly Gly Val Val	Ala Val Val Val Phe	Ala Met Leu Cys Leu	Leu		
	380	385	390		
Ile Ile Leu Gly	Arg Tyr Phe Ala Arg	His Lys Gly Thr Tyr	Phe		
	395	400	405		
Thr His Glu Ala	Lys Gly Ala Asp Asp	Ala Ala Asp Ala Asp	Thr		
	410	415	420		
Ala Ile Ile Asn	Ala Glu Gly Gly Gln	Asn Asn Ser Glu Glu	Lys		
	425	430	435		
Lys Glu Tyr Phe	Ile				
	440				

<210> 62
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 62
 ggcttctgct gttgctcttc tccg 24

<210> 63
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 63
 gtacactgtg accagtcagc 20

<210> 64
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
ggggcggtg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50
cctcgggccc gaccgcag gaaagactga ggccgcggcc tgccccgccc 100
ggctccctgc gccgcgcgcg cctcccggga cagaagatgt gctccagggt 150
ccctctgctg ctgcgctgc tctgctact ggccctgggg cctgggggtgc 200
agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250
actgcccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggc 300
ggggctgtac gtctttgaga acggcatcac catgctcgac gcaagcagct 350
ttgccggcct gccgggctg cagctcctgg acctgtcaca gaaccagatc 400

gccagcctgc gcctgccccg cctgctgctg ctggacctca gccacaacag 450
 cctcctggcc ctggagcccc gcctcctgga cactgccaac gtggaggcgc 500
 tgcggctggc tggctctggg ctgcagcagc tggacgaggg gctcttcagc 550
 cgcttgcgca acctccacga cctggatgtg tccgacaacc agctggagcg 600
 agtgccacct gtgatccgag gcctccgggg cctgacgcgc ctgaggctgg 650
 ccggcaacac ccgcattgcc cagctgcggc ccgaggacct ggccggcctg 700
 gctgccctgc aggagctgga tgtgagcaac ctaagcctgc aggcctgcc 750
 tggcgacctc tcgggcctct tccccgcct gcggctgctg gcagctgcc 800
 gcaaccctt caactgcgtg tgccccctga gctggtttg cccctgggtg 850
 cgcgagagcc acgtcacact ggccagccct gaggagacgc gctgccactt 900
 cccgcccaag aacgctggcc ggctgctcct ggagcttgac tacgccgact 950
 ttggctgccc agccaccacc accacagcca cagtgccac cacgaggccc 1000
 gtggtgcggg agccacagc cttgtcttct agcttggtc ctacctggt 1050
 tagccccaca gcgcgggcca ctgaggcccc cagcccgccc tccactgcc 1100
 caccgactgt agggcctgtc cccagcccc aggactgccc accgtccacc 1150
 tgctcaatg ggggcacatg ccacctgggg acaaggcacc acctggcggtg 1200
 cttgtgcccc gaaggcttca cgggcctgta ctgtgagagc cagatggggc 1250
 aggggacacg gcccagccct acaccagtca cgccgaggcc accacgggtc 1300
 ctgacctggt gcctcgagcc ggtgagcccc acctccctgc gcgtggggct 1350
 gcagcgtac ctccagggga gctccgtgca gctcaggagc ctccgtctca 1400
 cctatcgcaa cctatcgggc cctgataagc ggctggtgac gctgagactg 1450
 cctgcctcgc tcgtgagta cacggtcacc cagctgcggc ccaacgccac 1500
 ttactccgtc tgtgtcatgc ctttggggcc cgggcgggtg ccggagggcg 1550
 aggaggcctg cggggaggcc cataaccccc cagccgtcca ctccaaccac 1600
 gccccagtca cccagggccc cgagggaac ctgccgctcc tcattgcgcc 1650
 cgccctggcc gcgggtgctc tggccgcgct ggctgcgggtg ggggcagcct 1700
 actgtgtgcg gcggggggcg gccatggcag cagcggctca ggacaaaggg 1750
 caggtggggc caggggctgg gccctggaa ctggagggag tgaaggctcc 1800
 cttggagcca ggcccgaagg caacagagg cggtggagag gccctgccca 1850

gcgggtctga	gtgtgagg	ccactcatgg	gcttcccagg	gcctggcctc	1900
cagtcacccc	tccacgcaa	gccctacatc	taagccagag	agagacaggg	1950
cagctggggc	cgggctctca	gccagtgaga	tggccagccc	cctcctgctg	2000
ccacaccacg	taagttctca	gtcccaacct	cggggatgtg	tgcagacagg	2050
gctgtgtgac	cacagctggg	ccctgttccc	tctggacctc	ggtctcctca	2100
tctgtgagat	gctgtggccc	agctgacgag	ccctaacgtc	cccagaaccg	2150
agtgccatat	aggacagtgt	ccgccctgcc	ctccgcaacg	tgcagtccct	2200
gggcacggcg	ggccctgcc	tgtgctggta	acgcatgcct	gggccctgct	2250
gggctctccc	actccaggcg	gaccctgggg	gccagtgaag	gaagctcccg	2300
gaaagagcag	agggagagcg	ggtaggcggc	tgtgtgactc	tagtcttggc	2350
cccaggaagc	gaaggaacaa	aagaaactgg	aaaggaagat	gctttaggaa	2400
catgttttgc	ttttttaaaa	tatatatata	tttataagag	atcctttccc	2450
atttattctg	ggaagatgtt	tttcaaactc	agagacaagg	actttggttt	2500
ttgtaagaca	aacgatgata	tgaaggcctt	ttgtaagaaa	aaataaaaaa	2550
aaaaa	2555				

```
<210> 69
<211> 598
<212> PRT
<213> Homo Sapien
```

				110						115				120
Ala	Leu	Arg	Leu	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly
				125						130				135
Leu	Phe	Ser	Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp
				140						145				150
Asn	Gln	Leu	Glu	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly
				155						160				165
Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu
				170						175				180
Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp
				185						190				195
Val	Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly
				200						205				210
Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe
				215						220				225
Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu
				230						235				240
Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe
				245						250				255
Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala
				260						265				270
Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr
				275						280				285
Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu
				290						295				300
Ala	Pro	Thr	Trp	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	Pro
				305						310				315
Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln
				320						325				330
Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys
				335						340				345
His	Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly
				350						355				360
Phe	Thr	Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg
				365						370				375
Pro	Ser	Pro	Thr	Pro	Val	Thr	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr
				380						385				390
Leu	Gly	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Gly	Leu
				395						400				405

Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415	420
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro	Asp Lys Arg Leu Val Thr
425	430	435
Leu Arg Leu Pro	Ala Ser Leu Ala Glu	Tyr Thr Val Thr Gln Leu
440	445	450
Arg Pro Asn Ala	Thr Tyr Ser Val Cys	Val Met Pro Leu Gly Pro
455	460	465
Gly Arg Val Pro	Glu Gly Glu Glu Ala	Cys Gly Glu Ala His Thr
470	475	480
Pro Pro Ala Val	His Ser Asn His Ala	Pro Val Thr Gln Ala Arg
485	490	495
Glu Gly Asn Leu	Pro Leu Leu Ile Ala	Pro Ala Leu Ala Ala Val
500	505	510
Leu Leu Ala Ala	Leu Ala Ala Val Gly	Ala Ala Tyr Cys Val Arg
515	520	525
Arg Gly Arg Ala	Met Ala Ala Ala Ala	Gln Asp Lys Gly Gln Val
530	535	540
Gly Pro Gly Ala	Gly Pro Leu Glu Leu	Glu Gly Val Lys Val Pro
545	550	555
Leu Glu Pro Gly	Pro Lys Ala Thr Glu	Gly Gly Gly Glu Ala Leu
560	565	570
Pro Ser Gly Ser	Glu Cys Glu Val Pro	Leu Met Gly Phe Pro Gly
575	580	585
Pro Gly Leu Gln	Ser Pro Leu His Ala	Lys Pro Tyr Ile
590	595	

<210> 70
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 70
 ccctccactg cccaccgac tg 22

<210> 71
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccaccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgcc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcactagga caaccttctt ccttctgca ccaactgccc tacccttacc 50
cgccccgcca cctccttgct acccactct tgaaaccaca gctgttgga 100
gggtccccag ctcatgccag cctcatctcc tttcttgcta gccccaaag 150
ggcctccagg caacatgggg ggcccagtc gagagccggc actctcagtt 200
gccctctggt tgagttgggg ggcagctctg ggggccgtgg cttgtgccat 250
ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300
gccggctgca ggggacagga ggcccctccc agaatgggga agggatatccc 350
tggcagagtc tcccggagca gaggctccgat gccctggaag cctgggagaa 400

tggggagaga	tcccgaaaa	ggagagcagt	gtcacccaa	aaacagaaga	450
agcagcactc	tgtcctgcac	ctggttccca	ttaacgccac	ctccaaggat	500
gactccgatg	tgacagaggt	gatgtggcaa	ccagctctta	ggcgtgggag	550
aggcctacag	gccaaggat	atggtgtccg	aatccaggat	gctggagttt	600
atctgctgta	tagccaggtc	ctgtttcaag	acgtgacttt	caccatgggt	650
caggtggtgt	ctcgagaagg	ccaaggaagg	caggagactc	tattccgatg	700
tataagaagt	atgccctccc	acccggaccg	ggcctacaac	agctgctata	750
gcgcaggtgt	cttccattta	caccaagggg	atattctgag	tgtcataatt	800
ccccgggcaa	gggcgaaact	taacctctct	ccacatggaa	ccttcctggg	850
gtttgtgaaa	ctgtgattgt	gttataaaaa	gtggctccca	gcttggaaga	900
ccagggtggg	tacatactgg	agacagccaa	gagctgagta	tataaaggag	950
agggaatgtg	caggaacaga	ggcatcttcc	tgggtttggc	tcccgttcc	1000
tcacttttcc	cttttcattc	ccacccccta	gactttgatt	ttacggatat	1050
cttgcttctg	ttccccatgg	agctccg	1077		

```
<210> 76
<211> 250
<212> PRT
<213> Homo Sapien
```


[illegible]

				110					115					120	
Ala	Arg	Gly	His	Thr 125	Gly	Pro	Lys	Gly	Gln 130	Lys	Gly	Ser	Met	Gly 135	
Ala	Pro	Gly	Glu	Arg 140	Cys	Lys	Ser	His	Tyr 145	Ala	Ala	Phe	Ser	Val 150	
Gly	Arg	Lys	Lys	Pro 155	Met	His	Ser	Asn	His 160	Tyr	Tyr	Gln	Thr	Val 165	
Ile	Phe	Asp	Thr	Glu 170	Phe	Val	Asn	Leu	Tyr 175	Asp	His	Phe	Asn	Met 180	
Phe	Thr	Gly	Lys	Phe 185	Tyr	Cys	Tyr	Val	Pro 190	Gly	Leu	Tyr	Phe	Phe 195	
Ser	Leu	Asn	Val	His 200	Thr	Trp	Asn	Gln	Lys 205	Glu	Thr	Tyr	Leu	His 210	
Ile	Met	Lys	Asn	Glu 215	Glu	Glu	Val	Val	Ile 220	Leu	Phe	Ala	Gln	Val 225	
Gly	Asp	Arg	Ser	Ile 230	Met	Gln	Ser	Gln	Ser 235	Leu	Met	Leu	Glu	Leu 240	
Arg	Glu	Gln	Asp	Gln 245	Val	Trp	Val	Arg	Leu 250	Tyr	Lys	Gly	Glu	Arg 255	
Glu	Asn	Ala	Ile	Phe 260	Ser	Glu	Glu	Leu	Asp 265	Thr	Tyr	Ile	Thr	Phe 270	
Ser	Gly	Tyr	Leu	Val 275	Lys	His	Ala	Thr	Glu 280	Pro					

```
<210> 79
<211> 24
<212> DNA
<213> Artificial Sequence
```

```
<400> 79
tacaggccca gtcaggacca gggg 24
```

<220>
<223> Synthetic oligonucleotide probe

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccgggtgctt gcgctgctgt gaccccggtg cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
gcggagcatt cgctgcggtc ctgcgcgaga ccccgcgcg gattcgccgg 50
tccttcccg cggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100
ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
gacaaaaact aaactgaaat ttaaaatgtt cttcggggga gaaggagct 250
tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300
agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350
gtcatctctt tctaaggga tcaaggcaa tgagcccgta tatacttcaa 400
ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450
gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500
acccaactgc tacctatctt tctgtcccaa cgaggagcc tgtccattga 550
aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600
ttgaccagaa atttgccaag ccaagagtta ccccggaag attctctctt 650
acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700
attattcaaa gccaccgat atctcatgga gagacacact ttctcagaag 750
tttgatcct cagatcacct ggagaaacta ttttaagatg atgaagcaag 800
tgcccagctc cttgcttata aggaaaaagg ccattctcag agttcacaat 850
tttctctga tcaagaaata gctcatctgc tgctgaaaa tgtgagtgcg 900
ctcccagcta cgggtggcag tgccttctca cataccacct cggtactcc 950
aaagcccgcc acccttctac ccaccaatgc ttcagtga ccttctggga 1000
cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050

094443 2244460

FOOEEBO"2E44660

Ile	Cys	Phe	Leu	Thr	Leu	Arg	Leu	Ser	Ala	Ser	Gln	Asn	Cys	Leu	
				20					25					30	
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu	
				35					40					45	
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln	
				50					55					60	
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly	
				65					70					75	
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala	
				80					85					90	
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala	
				95					100					105	
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile	
				110					115					120	
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu	
				125					130					135	
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val	
				140					145					150	
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp	
				155					160					165	
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp	
				170					175					180	
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu	
				185					190					195	
Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser	
				200					205					210	
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala	
				215					220					225	
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala	
				230					235					240	
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr	
				245					250					255	
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro	
				260					265					270	
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr	
				275					280					285	
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr	
				290					295					300	
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly	

				305					310					315
Ser	Leu	Glu	Thr	Ile	Pro	Phe	Thr	Glu	Ile	Ser	Asn	Leu	Thr	Leu
				320					325					330
Asn	Thr	Gly	Asn	Val	Tyr	Asn	Pro	Thr	Ala	Leu	Ser	Met	Ser	Asn
				335					340					345
Val	Glu	Ser	Ser	Thr	Met	Asn	Lys	Thr	Ala	Ser	Trp	Glu	Gly	Arg
				350					355					360
Glu	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Gln	Gly	Ser	Val	Pro	Glu	Asn
				365					370					375
Gln	Tyr	Gly	Leu	Pro	Phe	Glu	Lys	Trp	Leu	Leu	Ile	Gly	Ser	Leu
				380					385					390
Leu	Phe	Gly	Val	Leu	Phe	Leu	Val	Ile	Gly	Leu	Val	Leu	Leu	Gly
				395					400					405
Arg	Ile	Leu	Ser	Glu	Ser	Leu	Arg	Arg	Lys	Arg	Tyr	Ser	Arg	Leu
				410					415					420
Asp	Tyr	Leu	Ile	Asn	Gly	Ile	Tyr	Val	Asp	Ile				
				425					430					

```
<210> 84
<211> 30
<212> DNA
<213> Artificial Sequence
```

[illegible]

<400> 87
caccqtaqct qggagcgcac tcac 24

<220>
<223> Synthetic oligonucleotide probe

```
<400> 88
  agtqtaagtc aaqctccc 18
```

```
<210> 89
<211> 49
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Synthetic oligonucleotide probe

<400> 89
gcttctctgac actaaggctg tctgctagtc agaattgcct caaaaagag 49

```
<210> 90
<211> 957
<212> DNA
<213> Homo Sapien
```

```
<400> 90
cctggaagat gcgcccattg gctggtggcc tgetcaaggt ggtgttcgtg 50
gtcttcgcct ccttgtgtgc ctggtattcg gggtaacctgc tcgcagagct 100
cattccagat gcacccctgt ccagtgtctgc ctatagcatc cgcagcatcg 150
gggagaggcc tgtcctcaaa gctccagtcc ccaaaaggca aaaatgtgac 200
cactggactc cctgcccatac tgacacctat gcctacaggt tactcagcgg 250
agggtggcaga agcaagtacg ccaaaatctg ctttgaggat aacctactta 300
tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350
aactatgtaa ctgggaatgt gacagcaaca cgatgttttg atatgtatga 400
aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450
aatccctgct cttcatqqtg acctatgacg acqaaagcac aagactqaat 500
```


aacgatgcc aagaatgccat agaagcactt ggaagtaaag aaatcaggaa 550
 catgaaattc aggtctagct gggatattat tgcagcaaaa ggcttggaac 600
 tcccttccga aattcagaga gaaaagatca accactctga tgctaagaac 650
 aacagatatt ctggctggcc tgcagagatc cagatagaag gctgcatacc 700
 caaagaacga agctgacact gcagggtcct gagtaaagt gttctgtata 750
 aacaaatgca gctggaatcg ctcaagaatc ttatttttct aaatccaaca 800
 gcccatatct gatgagtatt ttgggtttgt tgtaaacc aa tgaacatttg 850
 ctagtgtat caaatcttgg tacgcagtat ttttatacca gtattttatg 900
 tagtgaagat gtcaattagc aggaaactaa aatgaatgga aattcttaaa 950
 aaaaaaa 957

<210> 91
 <211> 235
 <212> PRT
 <213> Homo Sapien

<400> 91
 Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
 1 5 10 15
 Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
 20 25 30
 Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
 35 40 45
 Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
 50 55 60
 Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
 65 70 75
 Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
 80 85 90
 Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
 95 100 105
 Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
 110 115 120
 Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
 125 130 135
 Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
 140 145 150
 Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
 155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
170 175 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
185 190 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
200 205 210

Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
215 220 225

Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
230 235

<210> 92

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

aatgtgacca ctggactccc 20

<210> 93

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aggcttgga ctccttc 18

<210> 94

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 94

aagattcttg agcgattcca gctg 24

<210> 95

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 95

aatccctgct cttcatggtg acctatgacg acggaagcac aagactg 47

TOPSECRET

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 96
ctcaagaagc acgcgtactg c 21

<210> 97
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
ccaacctcag cttccgctc tacga 25

<210> 98
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
catccaggct cgccactg 18

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 99
tggcaaggaa tgggaacagt 20

<210> 100
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 100
atgctgccag acctgatcgc agaca 25

<210> 101
<211> 19
<212> DNA

TOOEO"2E44660

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 101

gggcagaaat ccagccact 19

<210> 102

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 102

cccttcgcct gcttttga 18

<210> 103

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gccatctaata tgaagcccat cttccca 27

<210> 104

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 104

ctggcggtgt cctctcctt 19

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cctcggtctc ctcactctgtg a 21

<210> 106

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

tggcccagct gacgagccct 20

<210> 107

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

ctcataggca ctcggttctg g 21

<210> 108

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108

tggtcccag cttggaaga 19

<210> 109

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

cagctcttgg ctgtctccag tatgtaccca 30

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

gatgcctctg ttctgcaca t 21

<210> 111

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

ggattctaatacgcactcactatagggctgc cgcgaacccc ttcaactg 48

<210> 112

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

ctatgaaatt aaccctcact aaagggaccg cagctgggtg accgtgta 48

<210> 113

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

ggattctaatacgcactcactatagggccgc cccgccacct cct 43

<210> 114

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

ctatgaaatt aaccctcact aaagggactc gagacaccac ctgaccca 48

<210> 115

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

ggattctaatacgcactcactatagggccca aggaaggcag gagactct 48

<210> 116

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 116

ctatgaaatt aaccctcact aaagggacta gggggtggga atgaaaag 48

<210> 117

<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 117
ggattctaatacgcactcactatagggccccctcgagctctcccgtgta 48

<210> 118
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 118
ctatgaaattaacccctcactaaaggggaaggctcgccactggtcgtaga 48

<210> 119
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 119
ggattctaatacgcactcactatagggcaaggagccgggacccaggaga 48

<210> 120
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 120
ctatgaaattaacccctcactaaagggagggggcccttggtgctgagt 47

FOOEEBO" aEttt60